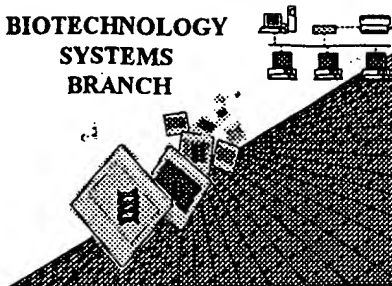




RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
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TECH CENTER 1600/2900

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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/554,945

Source: OPE

Date Processed by STIC: 9/6/2001

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TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



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OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/554,945

DATE: 09/06/2001
TIME: 15:07:52

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\09062001\I554945.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: CHEN, JIA-LUN
5 FU, GANG
6 SONG, HUAI-DONG
8 <120> TITLE OF INVENTION: A HUMAN HSG III GENE
11 <130> FILE REFERENCE: CPA-100US
13 <140> CURRENT APPLICATION NUMBER: 09/554,945
14 <141> CURRENT FILING DATE: 2001-08-20
16 <150> PRIOR APPLICATION NUMBER: PCT/CN98/00199
17 <151> PRIOR FILING DATE: 1998-09-22
19 <160> NUMBER OF SEQ ID NOS: 2
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2017
25 <212> TYPE: DNA
26 <213> ORGANISM: HOMO SAPIENS
W--> 27 <220> FEATURE: FEATURE
W--> 27 ~~<220> FEATURE: FEATURE~~ *delete - do not insert an alphabetical heading*
28 <221> NAME/KEY: UNSURE *when using new*
29 <222> LOCATION: (1930)(1990)(2005) *Sequence header*
30 <223> OTHER INFORMATION: ~~OTHER INFORMATION~~ cDNA Sequence *format.*
32 <400> SEQUENCE: 1 *delete*

33	taaagctacg	ccctggcgcg	agtctccgcg	tcacaggaac	ttcagcaccc	acagggcgga	60
34	cagcgctccc	ctctacctgg	agacttgact	cccgcgcgcc	ccaaccctgc	ttatcccttg	120
35	accgtcgagt	gtcagagatc	ctgcagccgc	ccagtcccg	cccctctccc	gccccacacc	180
36	caccctcctg	gctcttcttg	tttttactcc	tccttttcat	tcataacaaa	agctacagct	240
37	ccaggagccc	agcgcggggc	tgtgacccaa	gccgagcgtg	gaagaatggg	gttctctggg	300
38	accggcactt	ggattctggt	gttagtgctc	cagattcaag	ctttcccca	acctggagga	360
39	agccaagaca	aatctctaca	taatagagaa	ttaagtgcag	aaagaccttt	gaatgaacag	420
40	attgctgaag	cagaagaaga	caagattaaa	aaaacatata	ctccagaaaa	caagccaggt	480
41	cagagcaact	attcttttgt	tgataacttg	aacctgctaa	gggcaataac	agaaaaggaa	540
42	aaaattgaga	aagaaagaca	atctataaga	agctcccac	ttgataataa	gttgaatgtg	600
43	gaagatgttg	attcaaccaa	gaatcgaaaa	ctgatcgatg	attatgactc	tactaagagt	660
44	ggattggatc	ataaatttca	agatgatcca	gatggtcttc	atcaactaga	cgggactcct	720
45	ttaaccgctg	aagacattgt	ccataaaaatc	gctgccagga	tttatgaaga	aaatgacaga	780
46	gccgtgtttg	acaagattgt	ttctaaacta	cttaatctcg	gccttatcac	agaaagccaa	840
47	gcacatacac	tggagatga	agtagcagag	gttttacaaa	aattaatctc	aaaggaagcc	900
48	aacaattatg	aggaggatcc	caataagccc	acaagctgga	ctgagaatca	ggctggaaaa	960
49	ataccagaga	aagtgactcc	aatggcagca	attcaagatg	gtcttgctaa	gggagaaaac	1020
50	gatgaaacag	tatctaacac	attaaccttg	acaaatggct	tggaaaggag	aactaaaacc	1080
51	tacagtgaag	acaactttag	ggacttccaa	tatttcccaa	atttctatgc	gctactgaaa	1140
52	agtattgatt	cagaaaaaga	agcaaaagag	aaagaaacac	tgattactat	catgaaaaca	1200
53	ctgattgact	ttgtgaagat	gatggtgaaa	tatggaacaa	tatctccaga	agaaggtggt	1260
54	tcctaccttg	aaaacttgga	tgaaatgatt	gctcttcaga	ccaaaaacaa	gctagaaaaa	1320
55	aatgctactg	acaatataag	caagcttttc	ccagcaccat	cagagaagag	tcatgaagaa	1380
56	acagacagta	ccaaggaaga	agcagctaag	atggaaaagg	aatatggaag	cttgaaggat	1440
57	tccacaaaag	atgataactc	caaccagga	ggaaagacag	atgaacccaa	aggaaaaaca	1500
58	gaagcctatt	tggaaagccat	cagaaaaaat	attgaatggt	tgaagaaaca	tgacaaaaag	1560

The CRF program inserts alphabetical headings for clarity.

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DATE: 09/06/2001

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Input Set : A:\Seqlist.txt

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59 ggaaataaag aagattatga cctttcaaag atgagagact tcatcaataa acaagctgat 1620
 60 gcttatgtgg agaaaggcat ccttgacaag gaagaagccg aggccatcaa gcgcatttat 1680
 61 agcagcctgt aaaaatggca aaagatccag gagtctttca actgtttcag aaaacataat 1740
 62 atagcttaaa acacttctaa ttctgtgatt aaaatttttt gacccaaggg ttattagaaa 1800
 63 gtgctgaatt tacagtagtt aaccttttac aagtgggttaa aacatagctt tcttcccgtta 1860
 64 aaaactatct gaaagtaaag ttgtatgtaa gctgagattt tgtatacagg aatccttatt 1920
 65 tctcatagn cttattatatt tataatcagg aatatgttgc tttggaaaaa gcctcttaat 1980
 66 gggctgaccc taaaaactca atccntcttc cactgtc 2017
 68 <210> SEQ ID NO: 2
 69 <211> LENGTH: 468
 70 <212> TYPE: PRT
 71 <213> ORGANISM: HOMO SAPIENS
 73 <400> SEQUENCE: 2
 74 Met Gly Phe Leu Gly Thr Gly Thr Trp Ile Leu Val Leu Val Leu Pro
 75 1 5 10 15
 76 Ile Gln Ala Phe Pro Lys Pro Gly Gly Ser Gln Asp Lys Ser Leu His
 77 20 25 30
 78 Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln Ile Ala Glu
 79 35 40 45
 80 Ala Glu Glu Asp Lys Ile Lys Lys Thr Tyr Pro Pro Glu Asn Lys Pro
 81 50 55 60
 82 Gly Gln Ser Asn Tyr Ser Phe Val Asp Asn Leu Asn Leu Leu Arg Ala
 83 65 70 75 80
 84 Ile Thr Glu Lys Glu Lys Ile Glu Lys Glu Arg Gln Ser Ile Arg Ser
 85 85 90 95
 86 Ser Pro Leu Asp Asn Lys Leu Asn Val Glu Asp Val Asp Ser Thr Lys
 87 100 105 110
 88 Asn Arg Lys Leu Ile Asp Asp Tyr Asp Ser Thr Lys Ser Gly Leu Asp
 89 115 120 125
 90 His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu Asp Gly Thr
 91 130 135 140
 92 Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Ala Arg Ile Tyr
 93 145 150 155 160
 94 Glu Glu Asn Asp Arg Ala Val Phe Asp Lys Ile Val Ser Lys Leu Leu
 95 165 170 175
 96 Asn Leu Gly Leu Ile Thr Glu Ser Gln Ala His Thr Leu Glu Asp Glu
 97 180 185 190
 98 Val Ala Glu Val Leu Gln Lys Leu Ile Ser Lys Glu Ala Asn Asn Tyr
 99 195 200 205
 100 Glu Glu Asp Pro Asn Lys Pro Thr Ser Trp Thr Glu Asn Gln Ala Gly
 101 210 215 220
 102 Lys Ile Pro Glu Lys Val Thr Pro Met Ala Ala Ile Gln Asp Gly Leu
 103 225 230 235 240
 104 Ala Lys Gly Glu Asn Asp Glu Thr Val Ser Asn Thr Leu Thr Leu Thr
 105 245 250 255
 106 Asn Gly Leu Glu Arg Arg Thr Lys Thr Tyr Ser Glu Asp Asn Phe Arg
 107 260 265 270
 108 Asp Phe Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Lys Ser Ile Asp
 109 275 280 285

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110 Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile Thr Ile Met Lys
111      290                      295                      300
112 Thr Leu Ile Asp Phe Val Lys Met Met Val Lys Tyr Gly Thr Ile Ser
113 305                      310                      315                      320
114 Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn Leu Asp Glu Met Ile Ala
115                      325                      330                      335
116 Leu Gln Thr Lys Asn Lys Leu Glu Lys Asn Ala Thr Asp Asn Ile Ser
117                      340                      345                      350
118 Lys Leu Phe Pro Ala Pro Ser Glu Lys Ser His Glu Glu Thr Asp Ser
119                      355                      360                      365
120 Thr Lys Glu Glu Ala Ala Lys Met Glu Lys Glu Tyr Gly Ser Leu Lys
121      370                      375                      380
122 Asp Ser Thr Lys Asp Asp Asn Ser Asn Pro Gly Gly Lys Thr Asp Glu
123 385                      390                      395                      400
124 Pro Lys Gly Lys Thr Glu Ala Tyr Leu Glu Ala Ile Arg Lys Asn Ile
125                      405                      410                      415
126 Glu Trp Leu Lys Lys His Asp Lys Lys Gly Asn Lys Glu Asp Tyr Asp
127                      420                      425                      430
128 Leu Ser Lys Met Arg Asp Phe Ile Asn Lys Gln Ala Asp Ala Tyr Val
129                      435                      440                      445
130 Glu Lys Gly Ile Leu Asp Lys Glu Glu Ala Glu Ala Ile Lys Arg Ile
131      450                      455                      460
132 Tyr Ser Ser Leu
133 465

```

VERIFICATION SUMMARY

DATE: 09/06/2001

PATENT APPLICATION: US/09/554,945

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Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\09062001\I554945.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:283 W: Missing Blank Line separator, <220> field identifier
L:27 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1